RAW SEQUENCE LISTING   DATE: 06/14/2001
PATENT APPLICATION: US/09/841,730   TIME: 15:41:04

Input Set : **N:\Crf3\RULE60\09841730.txt**
Output Set: **N:\CRF3\06142001\I841730.raw**

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 4 <110> APPLICANT: Lee, Se-Jin
 5         McPherron, Alexandra C.
 7 <120> TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
 8         AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
11 <130> FILE REFERENCE: JHU1470-2
13 <140> CURRENT APPLICATION NUMBER: 09/841,730
14 <141> CURRENT FILING DATE: 2001-04-24
16 <150> PRIOR APPLICATION NUMBER: 09/626,896
17 <151> PRIOR FILING DATE: 2000-07-27
19 <150> PRIOR APPLICATION NUMBER: 09/485,046
20 <151> PRIOR FILING DATE: 2000-01-31
22 <150> PRIOR APPLICATION NUMBER: PCT/US98/15598
23 <151> PRIOR FILING DATE: 1998-07-28
25 <150> PRIOR APPLICATION NUMBER: 60/054,461
26 <151> PRIOR FILING DATE: 1997-08-01
28 <160> NUMBER OF SEQ ID NOS: 29
30 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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33 <211> LENGTH: 2743
34 <212> TYPE: DNA
35 <213> ORGANISM: Homo sapiens
37 <220> FEATURE:
38 <221> NAME/KEY: CDS
39 <222> LOCATION: (59)...(1183)
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43 atg caa aaa ctg caa ctc tgt gtt tat att tac ctg ttt atg ctg att      106
44 Met Gln Lys Leu Gln Leu Cys Val Tyr Ile Tyr Leu Phe Met Leu Ile
45  1               5                   10                  15
47 gtt gct ggt cca gtg gat cta aat gag aac agt gag caa aaa gaa aat      154
48 Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
49               20                  25                  30
51 gtg gaa aaa gag ggg ctg tgt aat gca tgt act tgg aga caa aac act      202
52 Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
53           35                  40                  45
55 aaa tct tca aga ata gaa gcc att aag ata caa atc ctc agt aaa ctt      250
56 Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
57       50                  55                  60
59 cgt ctg gaa aca gct cct aac atc agc aaa gat gtt ata aga caa ctt      298
60 Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Val Ile Arg Gln Leu
61   65                  70                  75                  80
63 tta ccc aaa gct cct cca ctc cgg gaa ctg att gat cag tat gat gtc      346
64 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
65               85                  90                  95
67 cag agg gat gac agc agc gat ggc tct ttg gaa gat gac gat tat cac      394
68 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
69              100                 105                 110
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71 gct aca acg gaa aca atc att acc atg cct aca gag tct gat ttt cta      442
72 Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu
73         115                 120                 125
75 atg caa gtg gat gga aaa ccc aaa tgt tgc ttc ttt aaa ttt agc tct      490
76 Met Gln Val Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
77      130                 135                 140
79 aaa ata caa tac aat aaa gta gta aag gcc caa cta tgg ata tat ttg      538
80 Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
81 145                 150                 155                 160
83 aga ccc gtc gag act cct aca aca gtg ttt gtg caa atc ctg aga ctc      586
84 Arg Pro Val Glu Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
85              165                 170                 175
87 atc aaa cct atg aaa gac ggt aca agg tat act gga atc cga tct ctg      634
88 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
89              180                 185                 190
91 aaa ctt gac atg aac cca ggc act ggt att tgg cag agc att gat gtg      682
92 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
93      195                 200                 205
95 aag aca gtg ttg caa aat tgg ctc aaa caa cct gaa tcc aac tta ggc      730
96 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
97      210                 215                 220
99 att gaa ata aaa gct tta gat gag aat ggt cat gat ctt gct gta acc      778
100 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
101 225                 230                 235                 240
103 ttc cca gga cca gga gaa gat ggg ctg aat ccg ttt tta gag gtc aag      826
104 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys
105              245                 250                 255
107 gta aca gac aca cca aaa aga tcc aga agg gat ttt ggt ctt gac tgt      874
108 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
109              260                 265                 270
111 gat gag cac tca aca gaa tca cga tgc tgt cgt tac cct cta act gtg      922
112 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
113      275                 280                 285
115 gat ttt gaa gct ttt gga tgg gat tgg att atc gct cct aaa aga tat      970
116 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
117      290                 295                 300
119 aag gcc aat tac tgc tct gga gag tgt gaa ttt gta ttt tta caa aaa     1018
120 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
121 305                 310                 315                 320
123 tat cct cat act cat ctg gta cac caa gca aac ccc aga ggt tca gca     1066
124 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
125              325                 330                 335
127 ggc cct tgc tgt act ccc aca aag atg tct cca att aat atg cta tat     1114
128 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
129              340                 345                 350
131 ttt aat ggc aaa gaa caa ata ata tat ggg aaa att cca gcg atg gta     1162
132 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
133         355                 360                 365
135 gta gac cgc tgt ggg tgc tca tgagatttat attaagcgtt cataacttcc         1213
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136 Val Asp Arg Cys Gly Cys Ser
137     370                 375
139 taaaacatgg aaggttttcc cctcaacaat tttgaagctg tgaaattaag taccacaggc   1273
140 tataggccta gagtatgcta cagtcactta agcataagct acagtatgta aactaaaagg   1333
141 gggaatatat gcaatggttg gcatttaacc atccaaacaa atcatacaag aaagttttat   1393
142 gatttccaga gttttttgagc tagaaggaga tcaaattaca tttatgttcc tatatattac   1453
143 aacatcggcg aggaaatgaa agcgattctc cttgagttct gatgaattaa aggagtatgc   1513
144 tttaaagtct atttctttaa agttttgttt aatatttaca gaaaaatcca catacagtat   1573
145 tggtaaaatg caggattgtt atataccatc attcgaatca tccttaaaca cttgaattta   1633
146 tattgtatgg tagtatactt ggtaagataa aattccacaa aaataggggat ggtgcagcat   1693
147 atgcaatttc cattcctatt ataattgaca cagtacatta acaatccatg ccaacggtgc   1753
148 taatacgata ggctgaatgt ctgaggctac caggtttatc acataaaaaa cattcagtaa   1813
149 aatagtaagt ttctcttttc ttcaggtgca tttttcctaca cctccaaatg aggaatggat   1873
150 tttctttaat gtaagaagaa tcattttttct agaggttggc tttcaattct gtagcatact   1933
151 tggagaaact gcattatctt aaaaggcagt caaatggtgt ttgtttttat caaaatgtca   1993
152 aaataacata cttggagaag tatgtaattt tgtctttgga aaattacaac actgcctttg   2053
153 caacactgca gtttttatgg taaaataata gaaatgatcg actctatcaa tattgtataa   2113
154 aaagactgaa acaatgcatt tatataatat gtatacaata ttgttttgta aataagtgtc   2173
155 tccttttttta tttactttgg tatattttta cactaaggac atttcaaatt aagtactaag   2233
156 gcacaaagac atgtcatgca tcacagaaaa gcaactactt atatttcaga gcaaattagc   2293
157 agattaaata gtggtcttaa aactccatat gttaatgatt agatggttat attacaatca   2353
158 ttttatattt ttttacatga ttaacattca cttatggatt catgatggct gtataaagtg   2413
159 aatttgaaat ttcaatggtt tactgtcatt gtgtttaaat ctcaacgttc cattatttta   2473
160 atacttgcaa aaacattact aagtatacca aaataattga ctctattatc tgaaatgaag   2533
161 aataaactga tgctatctca acaataactg ttacttttat tttataattt gataatgaat   2593
162 atatttctgc atttatttac ttctgttttg taaattggga ttttgttaat caaatttatt   2653
163 gtactatgac taaatgaaat tatttcttac atctaatttg tagaaacagt ataagttata   2713
164 ttaaagtgtt ttcacatttt tttgaaagac                                     2743
166 <210> SEQ ID NO: 2
167 <211> LENGTH: 375
168 <212> TYPE: PRT
169 <213> ORGANISM: Homo sapiens
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175             20                  25                  30
176 Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
177         35                  40                  45
178 Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
179     50                  55                  60
180 Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Val Ile Arg Gln Leu
181 65                  70                  75                  80
182 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
183             85                  90                  95
184 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
185             100                 105                 110
186 Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu
187         115                 120                 125
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188 Met Gln Val Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
189     130                 135                 140
190 Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
191 145               150               155               160
192 Arg Pro Val Glu Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
193             165               170               175
194 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
195           180               185               190
196 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
197         195               200               205
198 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
199     210               215               220
200 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
201 225               230               235               240
202 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys
203             245               250               255
204 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
205             260               265               270
206 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
207         275               280               285
208 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
209     290               295               300
210 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
211 305               310               315               320
212 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
213             325               330               335
214 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
215             340               345               350
216 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
217         355               360               365
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223 <212> TYPE: DNA
224 <213> ORGANISM: Mus musculus
226 <220> FEATURE:
227 <221> NAME/KEY: CDS
228 <222> LOCATION: (104)...(1231)
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232 aaataagaac aagggaaaaa aaaagattgt gctgattttt aaa atg atg caa aaa     115
233                                                 Met Met Gln Lys
234                                                  1
236 ctg caa atg tat gtt tat att tac ctg ttc atg ctg att gct gct ggc     163
237 Leu Gln Met Tyr Val Tyr Ile Tyr Leu Phe Met Leu Ile Ala Ala Gly
238  5                 10                  15                  20
240 cca gtg gat cta aat gag ggc agt gag aga gaa gaa aat gtg gaa aaa     211
241 Pro Val Asp Leu Asn Glu Gly Ser Glu Arg Glu Glu Asn Val Glu Lys
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242                   25                    30                      35
244 gag ggg ctg tgt aat gca tgt gcg tgg aga caa aac acg agg tac tcc    259
245 Glu Gly Leu Cys Asn Ala Cys Ala Trp Arg Gln Asn Thr Arg Tyr Ser
246               40                    45                    50
248 aga ata gaa gcc ata aaa att caa atc ctc agt aag ctg cgc ctg gaa    307
249 Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu Arg Leu Glu
250           55                    60                    65
252 aca gct cct aac atc agc aaa gat gct ata aga caa ctt ctg cca aga    355
253 Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu Leu Pro Arg
254       70                    75                    80
256 gcg cct cca ctc cgg gaa ctg atc gat cag tac gac gtc cag agg gat    403
257 Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val Gln Arg Asp
258 85                    90                    95                    100
260 gac agc agt gat ggc tct ttg gaa gat gac gat tat cac gct acc acg    451
261 Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His Ala Thr Thr
262                   105                   110                   115
264 gaa aca atc att acc atg cct aca gag tct gac ttt cta atg caa gcg    499
265 Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu Met Gln Ala
266               120                   125                   130
268 gat ggc aag ccc aaa tgt tgc ttt ttt aaa ttt agc tct aaa ata cag    547
269 Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser Lys Ile Gln
270           135                   140                   145
272 tac aac aaa gta gta aaa gcc caa ctg tgg ata tat ctc aga ccc gtc    595
273 Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu Arg Pro Val
274       150                   155                   160
276 aag act cct aca aca gtg ttt gtg caa atc ctg aga ctc atc aaa ccc    643
277 Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu Ile Lys Pro
278 165                   170                   175                   180
280 atg aaa gac ggt aca agg tat act gga atc cga tct ctg aaa ctt gac    691
281 Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu Lys Leu Asp
282               185                   190                   195
284 atg agc cca ggc act ggt att tgg cag agt att gat gtg aag aca gtg    739
285 Met Ser Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val Lys Thr Val
286               200                   205                   210
288 ttg caa aat tgg ctc aaa cag cct gaa tcc aac tta ggc att gaa atc    787
289 Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly Ile Glu Ile
290           215                   220                   225
292 aaa gct ttg gat gag aat ggc cat gat ctt gct gta acc ttc cca gga    835
293 Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr Phe Pro Gly
294       230                   235                   240
296 cca gga gaa gat ggg ctg aat ccc ttt tta gaa gtc aag gtg aca gac    883
297 Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys Val Thr Asp
298 245                   250                   255                   260
300 aca ccc aag agg tcc cgg aga gac ttt ggg ctt gac tgc gat gag cac    931
301 Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys Asp Glu His
302               265                   270                   275
304 tcc acg gaa tcc cgg tgc tgc cgc tac ccc ctc acg gtc gat ttt gaa    979
305 Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp Phe Glu
306               280                   285                   290
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VERIFICATION SUMMARY
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L:1721 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21